

Reference haplotypes

h_1	1	1	0	0	1	0
h_2	1	1	0	0	1	0
h_3	1	1	0	0	1	0
h_4	1	0	1	0	0	1
h_5	1	0	1	0	0	1
h_6	1	0	1	0	0	1
h_7	0	0	0	0	0	1
h_8	0	0	0	0	0	1

Target genotype

x_1	2	1	?	0	?	1
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1. Find unique haplotypes

2. Initialize missings

Unique reference haplotypes

h_1	1	1	0	0	1	0
h_4	1	0	1	0	0	1
h_7	0	0	0	0	0	1

$$\|x'_1 - h_1 - h_4\|^2 = 2$$

$$\|x'_1 - h_1 - h_7\|^2 = 2$$

$$\|x'_1 - h_4 - h_7\|^2 = 3$$

3. Find (possibly many) haplotype pairs using BLAS3 with least squares objective

$$x'_1 \approx h_1 + h_4$$

$$x'_1 \approx h_1 + h_7$$

4. R-calculating error on x_1 instead of x'_1 :

$$\|x_1 - h_1 - h_4\|^2 = 0$$

$$\|x_1 - h_1 - h_7\|^2 = 1$$

x_1 's optimal hap-pair(s)
 $= (h_1, h_4)$

5. Find all matching haplotypes in original reference panel

$$h_1 = h_2 = h_3$$

$$h_4 = h_5 = h_6$$

6. Form

Candidate haplotype pairs

$(h_1, h_4), (h_1, h_4), (h_1, h_6)$

$(h_2, h_4), (h_2, h_4), (h_2, h_6)$

$(h_3, h_4), (h_3, h_4), (h_3, h_6)$